



PCT

## RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/719,533A

TIME: 14:24:29

Input Set : A:\U013108-9sequence.txt

Output Set: N:\CRF4\04032003\I719533A.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gan, Chong Jin  
 6 Lin, Gek Heow  
 7 Leong, Ai Lin  
 8 Ngao, Yi  
 9 Chen, Wei Ning

11 (ii) TITLE OF INVENTION: A VACCINE-INDUCED HEPATITIS B VIRAL  
 12 CTFAIN AND USES THEREOF

14 (iii) NUMBER OF SEQUENCES: 11

16 (iv) CORRESPONDING ADDRESSES:

17 (A) ADDRESS: Lagan & Parry  
 18 (B) STREET: 16 West 61 Street  
 19 (C) CITY: New York  
 20 (D) STATE: New York  
 21 (E) COUNTRY: USA  
 22 (F) ZIP: 10003

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk  
 26 (B) COMPUTER: IBM PC compatible  
 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/719,533A  
 C--> 32 (B) FILING DATE: 13-Dec-2000  
 33 (C) CLASSIFICATION: 485

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: PCT/SG98/00045  
 37 (B) FILING DATE: 19-JUN-1998

39 (viii) ATTORNEY/AGENCY INFORMATION:

40 (A) NAME: Miller, Cynthia R.  
 41 (B) REGISTRATION NUMBER: 34,678  
 42 (C) REFERENCE/DOCKET NUMBER: U-013108-9

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (212) 703-1890

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 6215 base pairs  
 51 (B) TYPE: nucleic acid  
 52 (C) STRANDEDNESS: double  
 53 (D) TOPOLOGY: circular

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

57 CTCCACCACT TTCCACAAA CTCTTCAAGA TCCAGAGTC AGGGCCCTGT ACTTTCCTGC

60

ENTERED

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59 TGGTGGCTTC AGTTCAGGAA CAGTCAGGAC TGCTCAGAAT ACTGTCTCTG CCATATCTTC 120
61 AATCTTATCG AAGACTGGGG ACCCTGTACG GAACATGGAG AACATCGCAT CAGGACTCTT 180
63 AGGACCCCTG CTGTGTTCAT AGGCGGGGTT TTCTTGTTCG AAAAAATCC TCACAATAGC 240
65 GCAGAGTCTA GATCTGTGCT GGAATCTCTT CAATTTCTTA GGGGGAAACG CCGTGTCTCT 300
67 TGGGCAAAAT TCGAGTCTCT AAATCTCTAG TCACTCAGCA ACCTGTTCTC CCGCAATCTG 360
69 TCGTGGTCTT CGTGGGATCT GTCTGCTGGG TCTTATCTTC TCTCTCTGCA TCGTCTCT 420
71 ATGTCTCTTC TCTTGTTCG TCTCTCTGCA CTATCAAGGT ATCTTGGGG TCTCTCTCT 480
73 AATTTCAGGA TCAACAGCAA CAGGACGG AGCATGCAAA ACCTGACAAA CTCTCTCTA 540
75 AGCAACCTCT ATCTTCTCTT CATCTCTCTG TACAAAACCT ACAGACAGAA ACTGCACTG 600
77 TATCTCTATC CACTATCTCT GGGCTTCTTC AAAATCTCTA TGAGAGTGG CTTCTCTCT 660
79 TTTCTCTCTG CTCTCTTCTT TATCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 720
81 TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 780
83 GAGTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 840
85 CACAAAAA AAAGATCTCTT ATATCTCTCTT AACCTCTCTT GATCTCTCTT TCTCTCTCT 900
87 GCTCTCTCTT CACAAAAA TATCTCTCTT AAAATCTCTT TCTCTCTCTT TCTCTCTCTT 960
89 GCAAAAGAGG CTATCTCTT GAAAGATCTT CAACGATCTT TGGGCTCTCTT GGGGCTCTCT 1020
91 GGGGCTCTCT CAGCAATCTT ATATCTCTCT TCAATCTCTT TATCTCTCTT TATCTCTCT 1080
93 AAAGAGGCTT TCTCTCTCTT CCAAACTCTT AAGCTCTCTT TAAGTAAACA GTATCTCTCT 1140
95 CTCTCTCTCT TCTCTCTCTT AAGCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCT 1200
97 ACTCTCTCTT GCTCTCTCTT AGGCTCTCTT CAGCTCTCTT GAACTCTCTT GCTCTCTCT 1260
99 CAGCTCTCTT CAGCTCTCTT CAGCTCTCTT TCTCTCTCTT GCACTCTCTT TCTCTCTCT 1320
101 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1380
103 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1440
105 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1500
107 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1560
109 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1620
111 TCAAGCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1680
113 TCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1740
115 TCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1800
117 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1860
119 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1920
121 AGAATCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 1980
123 TCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2040
125 TCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2100
127 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2160
129 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2220
131 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2280
133 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2340
135 CTCTCTCTT CTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCT 2400

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157 TGGCCGGACG CCAACAAGGT GGGAGTGGGA GCATTGGGGC CAGGGTTCAC CCTCCTCAT 3060
158 GGGGGACTGT TGGGGTGGAG CCTCAGCT CAGGGCTAC TCACAACGTG GCCAGTAGCT 3120
159 CCTCCTCCTG CCTCCACCAA TCAGCACTCA GGAAGGCAGC CTACTCCTT ATCTCCAGCT 3180
160 CTAAGGGACA CTCATCTCA GCCATGACAG TGGAA 3215
161 (2) INFORMATION FOR SEQ ID NO: 2:
162 (i) SEQUENCE CHARACTERISTICS:
163 (A) LENGTH: 843 amino acids
164 (B) TYPE: amino acid
165 (C) STRANDEDNESS: single
166 (D) TOPOLOGY: linear
167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
168 Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Glu
169 1 5 10 15
170 Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
171 20 25 30
172 Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
173 35 40 45
174 Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
175 50 55 60
176 Ser Thr Val Pro Cys Phe Asn Pro Lys Trp Gln Thr Pro Ser Phe Pro
177 65 70 75 80
178 Asp Ile His Leu Gln Glu Asp Ile Leu Asp Arg Cys Lys Gln Phe Val
179 85 90 95
180 Glu Pro Leu Thr Val Asn Glu Asn Arg Arg Leu Lys Leu Ile Met Pro
181 100 105 110
182 Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
183 115 120 125
184 Ile Lys Pro Tyr Tyr Pro Glu Tyr Val Val Asn His Tyr Pro Gln Thr
185 130 135 140
186 Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
187 145 150 155 160
188 Gln Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
189 165 170 175
190 Gln Asp Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Lys Arg His
191 180 185 190
192 Gly Asp Lys Ser Phe Cys Pro Glu Ser Pro Gly Ile Leu Pro Arg Ser
193 195 200 205
194 Ser Val Gly Pro Cys Ile Gln Ser Gln Leu Arg Lys Ser Arg Leu Gly
195 210 215 220
196 Pro Gln Pro Ala Gln Gly Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser
197 225 230 235 240
198 Gly Ser Ile Arg Ala Arg Val His Pro Ser Ser Trp Gly Thr Val Gly
199 245 250 255
200 Val Glu Pro Ser Gly Ser Gly Pro Thr His Asn Cys Ala Ser Ser Ser
201 260 265 270
202 Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser Leu
203 275 280 285
204 Ile Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val Glu Leu
205 290 295 300

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225	His	His	Phe	Pro	Pro	Asn	Ser	Ser	Arg	Ser	Gln	Ser	Gln	Gly	Pro	Val
230	305					310				315						320
235	Leu	Ser	Cys	Trp	Trp	Leu	Gln	Phe	Arg	Asn	Ser	Glu	Pro	Cys	Ser	Glu
239				325						330						335
241	Tyr	Cys	Leu	Cys	His	Ile	Val	Asn	Leu	Ile	Glu	Asp	Trp	Gly	Pro	Cys
241				340					345						350	
244	Thr	Glu	His	Gly	Glu	His	Arg	Ile	Arg	Thr	Pro	Arg	Thr	Pro	Ala	Arg
248				355					360						365	
249	Val	Thr	Gly	Gly	Val	Phe	Leu	Val	Asp	Lys	Asn	Pro	His	Asn	Thr	Ala
249				370					375						380	
250	Glu	Ser	Arg	Leu	Val	Val	Asp	Phe	Ser	Gln	Phe	Ser	Arg	Gly	Asn	Thr
251	385					390					395					400
255	Arg	Val	Ser	Trp	Pro	Lys	Phe	Ala	Val	Pro	Asn	Leu	Gln	Ser	Leu	Thr
254				405						410						415
256	Asn	Leu	Leu	Ser	Ser	Asn	Leu	Ser	Trp	Leu	Ser	Leu	Asp	Val	Ser	Ala
257				415						420						425
259	Ala	Phe	Tyr	His	Leu	Pro	Leu	His	Pro	Ala	Ala	Met	Pro	His	Leu	Leu
261				435					440							445
262	Val	Gly	Ser	Ser	Gly	Leu	Ser	Arg	Tyr	Val	Ala	Arg	Leu	Ser	Ser	Asn
263				450					455							460
267	Ser	Arg	Ile	Asn	Asn	Asn	Glu	His	Arg	Thr	Met	Glu	Asn	Leu	His	Asn
266	465					470					475					480
268	Ser	Cys	Ser	Arg	Asn	Leu	Tyr	Val	Ser	Leu	Met	Leu	Leu	Tyr	Lys	Thr
269				485						490						495
271	Tyr	Gly	Gln	Lys	Leu	His	Leu	Tyr	Ser	His	Pro	Ile	Ile	Leu	Gly	Phe
271				500						505						510
274	Arg	Lys	Ile	Pro	Met	Gly	Val	Gly	Leu	Ser	Pro	Phe	Leu	Leu	Ala	Gln
273				515					520							525
277	Phe	Thr	Ser	Ala	Ile	Cys	Ser	Val	Val	Arg	Arg	Ala	Phe	Pro	His	Cys
278				530					535							540
280	Leu	Ala	Phe	Ser	Tyr	Met	Asp	Asp	Val	Val	Leu	Gly	Ala	Lys	Ser	Val
281	545					550					555					560
282	Gln	His	Leu	Gln	Ser	Leu	Tyr	Ala	Ala	Val	Thr	Asn	Phe	Leu	Leu	Ser
284				565						570						575
288	Leu	Gly	Ile	His	Leu	Asn	Pro	His	Lys	Thr	Lys	Arg	Trp	Gly	Tyr	Ser
287				580					585							590
289	Leu	Asn	Phe	Met	Gly	Tyr	Val	Ile	Gly	Ser	Trp	Gly	Thr	Leu	Pro	Gln
290				595					600							605
296	Glu	His	Ile	Val	Gln	Lys	Ile	Lys	Met	Cys	Phe	Arg	Lys	Leu	Pro	Val
298				610					615							620
299	Asn	Arg	Pro	Ile	Asp	Trp	Lys	Val	Cys	Gln	Arg	Ile	Val	Gly	Leu	Leu
300	625					630					635					640
302	Gly	Phe	Ala	Ala	Pro	Phe	Thr	Gln	Cys	Gly	Tyr	Pro	Ala	Leu	Met	Pro
303				645						650						655
305	Leu	Tyr	Ala	Cys	Ile	Gln	Ala	Lys	Gln	Ala	Phe	Thr	Phe	Ser	Gln	Thr
305				660					665							670
309	Tyr	Lys	Thr	Phe	Leu	Ser	Lys	Gln	Tyr	Leu	Asn	Leu	Tyr	Pro	Val	Ala
309				675					680							685
308	Arg	Gln	Arg	Pro	Gly	Leu	Cys	Glu	Val	Phe	Ala	Asp	Ala	Thr	Pro	Thr

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```

309          690          695          700
311 Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr Phe Val
312 705          710          715          720
314 Ser Pro Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala
315          725          730          735
317 Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
318          740          745          750
320 Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
321          755          760          765
323 Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
324          770          775          780
326 Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
327          785          790          795          300
329 Leu Leu Arg Leu Leu Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
330          800          810          815
332 Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe
333          820          825          830
335 Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
336          835          840
340 (2) INFORMATION FOR SEQ ID NO: 3:
341 (i) SEQUENCE CHARACTERISTICS:
342 (A) LENGTH: 400 amino acids
343 (B) TYPE: amino acid
344 (C) STRANDEDNESS: single
345 (D) TOPOLOGY: linear
346 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
347 Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
348 1 5 10 15
349 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
350 20 25 30
351 Ala Phe Lys Ala Asn Ser Gln Asn Pro Asp Trp Asp Leu Asn Pro His
352 35 40 45
353 Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly
354 50 55 60
355 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
356 65 70 75 80
357 Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
358 85 90 95
359 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
360 100 105 110
361 Arg Asp Thr His Pro Gln Ala Met Gln Trp Asp Ser Thr Thr Phe His
362 115 120 125
363 Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly
364 130 135 140
365 Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala
366 145 150 155 160
367 Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn Met Glu
368 165 170 175
369 Asn Ile Ala Ser Gly Leu Leu Gly Pro Leu Leu Val Leu Gln Ala Gly

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## VERIFICATION SUMMARY

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Input Set : A:\U013108-9sequence.txt

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]